

- O I P E  
SEP 09 2003  
PATENT & TRADEMARK OFFICE
- (1) GENERAL INFORMATION:  
(i) APPLICANT: Simons, Michael  
Volk, Rudiger  
Horowitz, Arie  
(ii) TITLE OF INVENTION: Stimulation of angiogenesis via enhanced endothelial expression of syndecan-4 core proteins  
(iii) NUMBER OF SEQUENCES: 24  
(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: David Prashker, Esq.  
(B) STREET: P.O. Box 5387  
(C) CITY: Magnolia  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 01930  
(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
(B) COMPUTER: Dell PC  
(C) OPERATING SYSTEM: MS DOS  
(D) SOFTWARE: Microsoft Word version 97  
(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/145,916  
(B) FILING DATE: September 2, 1998  
(C) CLASSIFICATION: Unknown  
(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: David Prashker, Esq.  
(B) REGISTRATION NUMBER: 29,693  
(C) REFERENCE/DOCKET NUMBER: BIS-039  
(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (978) 525-3794
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 762 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGACGTG CGCGCTCTG GCTTGGCTC TGCGCGCTGG CGCTGCGCCT GCAGCCTGCC 60  
CTCCCGAAA TTGTCACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGGACGAC 120  
TCAGACAAC TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180  
ACACCTTCCA CTGGAAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240  
ACCAGCAGGG ATACCGAGGC CACCCCTCAC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300  
GAGGGAGAGC CCGTGGCCCA CGTGGAAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG 360  
AAGGAGGCCA CCACCAAGGC TAGGGAGACC ACACAGCTCC CAGTCACCCA ACAGGCCTCA 420  
ACAGCAGCCA GAGCCACCA GGGCCAGGCA TCTGTACCGT CTCATCCCCA CGGGGATGTG 480  
CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540  
CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAAGAGG TTGTGGAGGA TGAAACTACC 600  
AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAGACT TCACCTTTGA AACATCTGGG 660  
GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720  
GGAGCCACAG GTGCTTCTCA GGGCCTTTG GACAGGAAGG AA 762

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1020 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG 60

GAGGCGCGGC GCGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGGACGC 120  
 GCTGCTCTCC AGATACCCCC GGAGCTCCAG CGCGCGGGAT CGCGCGCTCC CGCCGCTCTG 180  
 CCCCTAAACT TCTGCCGTAG CTCCCTTCAG AGCCAGCGAA TTTATTCCCTT AAAACCAGAA 240  
 ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACACAGCA GAGCAAGAAG 300  
 AGCTTCAGAG AGCAGCCTTC CGGGAGCACC AACTCCGTG TGCGGGTGCA GAAACCAACA 360  
 AGTGAGAGGG CGCCGCGTTC CGGGGGCGCA GCTGCGGGCG GCAGGAGCAG GCGCAGGAGG 420  
 AGGAAGCGAG CGCCCCCGAG CCCCAGGCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480  
 GGTACTCTGC TCCGGATTAG TGTCGCGGG CTCGCGAGC GCTGGGCAGG AGGCTTCGTT 540  
 TTGCCCTGGT TGCAAGCAGC GGCTGGGAGC AGCCGGTCCC TGGGAATAT GCGGCGCGCG 600  
 TGGATCTGC TCACCTGGG CTTGGTGGCC TGCGTGTGG CGGAGTCGAG AGCAGAGCTG 660  
 ACATCTGATA AAGACATGTA CCTTGACAAC AGCTCCATTG AAGAACGCTTC AGGAGTGTAT 720  
 CCTATTGATG ACAGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780  
 AGTCCAGAGC TGACAACAAAC TCGACCACTT CCAAAGATAC TGTTGACTAG TGCTGCTCCA 840  
 AAAGTGGAAA CCACGACGCT GAATATACAG ACAAGATAC CTGCTCAGAC AAAGTCACCT 900  
 GAAGAAACTG ATAAAGAGAA AGTTCACCTC TCTGACTCAG AAAGGAAAAT GGACCCAGCC 960  
 GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTAA ACGGACAGAA 1020

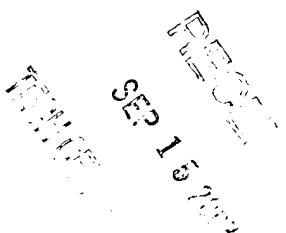
(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Arg Arg Glu Gly Ala Arg Gly Lys Glu Glu Glu Glu Lys Glu Glu  
 1 5 10 15  
 Asp Pro Gly Arg Glu Ala Arg Arg Gly Arg Arg Arg Gly Ala Ala Ala  
 20 25 30  
 Glu Pro Val Ala Pro Leu Gly Arg Ala Ala Leu Gln Ile Pro Pro Glu  
 35 40 45  
 Leu Gln Pro Arg Gly Ser Arg Ala Pro Ala Ala Leu Pro Leu Asn Phe  
 50 55 60  
 Cys Arg Ser Ser Leu Ser Ser Gln Arg Ile Tyr Ser Leu Lys Pro Glu  
 65 70 75 80  
 Thr Glu Pro Arg His Gly Lys Gly Val Arg Gly Gly Ala Lys Pro Gln  
 85 90 95  
 Gln Ser Lys Lys Ser Phe Arg Glu Gln Pro Ser Arg Ser Thr Asn Ser  
 100 105 110  
 Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg  
 115 120 125  
 Gly Ala Ala Ala Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala  
 130 135 140  
 Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys  
 145 150 155 160  
 Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala  
 165 170 175  
 Gly Gly Phe Val Pro Trp Leu Gln Ala Ala Gly Ser Ser Arg  
 180 185 190  
 Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu  
 195 200 205  
 Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys  
 210 215 220  
 Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr  
 225 230 235 240  
 Pro Ile Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp  
 245 250 255  
 Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Arg Pro Leu Pro Lys  
 260 265 270  
 Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Leu Asn  
 275 280 285



Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp  
 290                    295                    300  
 Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala  
 305                    310                    315                    320  
 Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe  
 325                    330                    335  
 Lys Arg Thr Glu  
 340

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1079 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCCCCCGCGC GCTGCTGAGC CGTCCTTGC G CACGSSGAT G CCGCGGGAG CTGCGGCC 60  
 TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120  
 AGAAACTACGA GAGGCCGGTG GACCTGGAGG GCTCTGGGGA TGATGATCCC TTTGGGGACG 180  
 ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240  
 TGGAGACAGC GGTCA GCGCTC ACCACGGACA CGTCCGTC CC ACTGCCACC ACGGTGGCCG 300  
 TGCTGCCTGT CACCTTGGTG CAGCCCCATGG CAACACCCCT TGAGCTGTT CCCACAGAGG 360  
 ACACGTCccc TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAG 420  
 TGATCCCCAG CTGGAAAACA ACCACCGCCA GTACCACTGC CAGTGA CTC CCCAGTACCA 480  
 CCTCCACCAC CACCACCA CACCACCA GCTGCTACCA CCACCA CACAC CACCA CACCA ATCAGCACCA 540  
 CTGTGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTCC GCCCCCTTT GTCACCAAGG 600  
 CAGCCACCA CCGGGCCACC ACCCTGGAGA CGCCCACCA CTCCATCCCT GAAACCAGTG 660  
 TCCTGACAGA GGTGACCA CTA CGGCTTG TCCCCTCCAG CACAGCCAAG CCGAGGTCCC 720  
 TGC CAA AAC ACC AAGCACTTCC AGGACTGCAG AACCCACGG AAAAAGCACT GCCTTGCTT 780  
 CCAGCCCCAC CACGCTGCCA CCCACAGAA G CCCCCCAGGT GGAGCCAGGG GAGTTGACGA 840  
 CAGTCCTCGA CAGTGA CTC GAAAGTCCCA CCAGTAGTGG CCC CAGCGGG GACTTCGAGA 900  
 TCCAGGAGGA GGAGGAGACA ACTCGCCTG AGCTGGGCAA TGAGGTGGTG GCAGTGGTGA 960  
 CACCACCA CAGCAGGGG CTGGGAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020  
 TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 447 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCGCCTG TCTGCCTGTT TGCGCCGCTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60  
 GCCCCAGGCG AGTCGATTG AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120  
 AGATACTTCT CTGGAGCCCT CCCGGACGAT GAAGACGCTG GGGGCCTTGA GCAGGACTCT 180  
 GACTTTGAGC TGTGGGTT CCGGAGATCTA GATGACACGG AGGAGCCAG GACCTTCCCT 240  
 GAGGTGATTT CACCCCTGGT GCCACTAGAT AACCA CACATCC CCGAGAATGC CCAGCCTGGC 300  
 ATCCGTGTCC CCTCAGAGCC CAAGGA CACTG GAAGAGAATG AGGTCA TCC CAAAGGGTC 360  
 CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCAG 420  
 GGCAGCAACA TTTTGAAAG AACTGAG                    447

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1590 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGCTCC	GGGCCCGAGG	CTGGTGGCTG	CTGTGCGCGG	CCGCCGCGCT	AGTCGCCTGC	60
GCCCCGGGG	ACCCGCCAG	CAAGAGCCG	AGCTGCAGCG	AAGTCGCCA	GATCTACGGG	120
GCTAAGGGCT	TTAGCCTGAG	CGACGTGCC	CAGGCAGAGA	TCTCGGGAGA	GCACCTGCGG	180
ATCTGCCCC	AGGGCTACAC	CTGCTGCACC	AGTGAGATGG	AGGAGAACCT	GGCCAACCAC	240
AGCCGGATGG	AGCTGGAGAC	CGCACTCCAC	GACAGCAGCC	GTGCCCTGCA	GGCTACACTG	300
GCCACCCAGC	TGCATGGCAT	CGATGACCAC	TTCCAGCGCC	TGCTGAATGA	CTCGGAGCGT	360
ACACTGCAGG	ATGCTTTCC	CGGGGCTTT	GGGGACCTGT	ACACGCAGAA	CACTCGGGCC	420
TTCCGGGACC	TGTATGCTGA	GCTGCCCTC	TACTACCGAG	GGGCCAACCT	ACACCTTGAG	480
GAGACACTGG	CCGAGTTCTG	GGCACGGCTG	CTGGAGCGTC	TCTTCAGCA	GCTGCACCCC	540
CAGCTTCTGC	TGCCCCATGA	CTATCTGGAC	TGCCTGGGCA	AGCAGGCAGA	GGCACTGCGG	600
CCGTTGGGG	ATGCCCTCG	AGAACTGCG	CTGAGGGCCA	CCCGTGCTT	TGTGGCGGCA	660
CGATCCTTTG	TGCAAGGGCCT	GGGTGTGGCC	AGTGACGTAG	TCCGAAAGGT	GGCCCAAGGTT	720
CCTCTGGCC	CAGAATGTT	TCGGGCTGTC	ATGAAGTTGG	TCTACTGTGC	CCATTGCCCG	780
GGAGTCCCTG	GTGCCCGGCC	CTGTCCCGAC	TATTGCCGAA	ATGTGCTCAA	AGGCTGCCCT	840
GCCAACCAGG	CCGACCTGGA	TGCCGAGTGG	AGGAACCTCC	TGGACTCCAT	GGTGCTCATC	900
ACTGACAAGT	TCTGGGGCCC	GTCGGGTGCG	GAGAATGTCA	TTGGCAGTGT	GCATATGTGG	960
CTGGCGGAGG	CCATCAACGC	CCTCCAGGAC	AACAAGGACA	CACTCACAGC	TAAGGTCATC	1020
CAGGGCTGCG	GAAACCCCAA	GGTCAATCCC	CATGGCTCTG	GGCCTGAGGA	GAAGCGTCGC	1080
CGTGGCAAAC	TGGCACTGCA	GGAGAAGTCC	TCCACAGGT	CTCTGGAAAA	GCTGGTCTCT	1140
GAGGCCAAGG	CCCAGCTCCG	AGACATTCA	GACTACTGGA	TCAGCCTCCC	AGGGACACTG	1200
TGTAGTGAGA	AGATGGCCAT	GAGTCCTGCC	AGCGATGACC	GCTGCTGGAA	TGGGATTTC	1260
AAGGGCCGGT	ACCTACCTGA	GGTGATGGGT	GATGGGCTGG	CCAACCAGAT	CAACAACCT	1320
GAAGTGGGAGG	TGGACATCAC	CAAGCCGGAT	ATGACCATCC	GGCAGCAGAT	CATGCAGCTC	1380
AAGATCATGA	CCAACCGTTT	ACGTGGCGCC	TACGGTGGCA	ATGATGTGGA	CTTCCAGGAT	1440
GCCAGTGATG	ACGGCAGTGG	CTCCGGCAGC	GTTGGCGGAT	GCCCAGATGA	CGCCTGTGGC	1500
CGGAGGGTCA	GCAAGAAGAG	CTCCAGCTCC	CGGACCCCC	TGACCCATGC	CCTCCCCGGC	1560
TTGTCAGAAC	AGGAGGGACA	GAAGACCTCG				1590

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Glu	Leu	Arg	Ala	Arg	Gly	Trp	Trp	Leu	Leu	Cys	Ala	Ala	Ala	Ala	Ala
1							5			10						15
Leu	Val	Ala	Cys	Ala	Arg	Gly	Asp	Pro	Ala	Ser	Lys	Ser	Arg	Ser	Cys	
								20		25						30
Ser	Glu	Val	Arg	Gln	Ile	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ser	Asp	
								35		40						45
Val	Pro	Gln	Ala	Glu	Ile	Ser	Gly	Glu	His	Leu	Arg	Ile	Cys	Pro	Gln	
								50		55						60
Gly	Tyr	Thr	Cys	Cys	Thr	Ser	Glu	Met	Glu	Glu	Asn	Leu	Ala	Asn	His	
								65		70						80
Ser	Arg	Met	Glu	Leu	Glu	Thr	Ala	Leu	His	Asp	Ser	Ser	Arg	Ala	Leu	
								85		90						95
Gln	Ala	Thr	Leu	Ala	Thr	Gln	Leu	His	Gly	Ile	Asp	Asp	His	Phe	Gln	
								100		105						110
Arg	Leu	Leu	Asn	Asp	Ser	Glu	Arg	Thr	Leu	Gln	Asp	Ala	Phe	Pro	Gly	
								115		120						125
Ala	Phe	Gly	Asp	Leu	Tyr	Thr	Gln	Asn	Thr	Arg	Ala	Phe	Arg	Asp	Leu	
								130		135						140
Tyr	Ala	Glu	Leu	Arg	Leu	Tyr	Tyr	Arg	Gly	Ala	Asn	Leu	His	Leu	Glu	
								145		150						160
Glu	Thr	Leu	Ala	Glu	Phe	Trp	Ala	Arg	Leu	Leu	Glu	Arg	Leu	Phe	Lys	
								165		170						175
Gln	Leu	His	Pro	Gln	Leu	Leu	Leu	Pro	Asp	Asp	Tyr	Leu	Asp	Cys	Leu	
								180		185						190
Gly	Lys	Gln	Ala	Glu	Ala	Leu	Arg	Pro	Phe	Gly	Asp	Ala	Pro	Arg	Glu	

195	200	205
Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala	Arg Ser Phe Val	
210	215	220
Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val		
225	230	235
Pro Leu Ala Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys		240
245	250	255
Ala His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys		
260	265	270
Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala		
275	280	285
Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe		
290	295	300
Trp Gly Pro Ser Gly Ala Glu Asn Val Ile Gly Ser Val His Met Trp		
305	310	315
Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Lys Asp Thr Leu Thr		320
325	330	335
Ala Lys Val Ile Gln Gly Cys Gly Asn Pro Lys Val Asn Pro His Gly		
340	345	350
Ser Gly Pro Glu Glu Lys Arg Arg Gly Lys Leu Ala Leu Gln Glu		
355	360	365
Lys Ser Ser Thr Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala		
370	375	380
Gln Leu Arg Asp Ile Gln Asp Tyr Trp Ile Ser Leu Pro Gly Thr Leu		
385	390	395
Cys Ser Glu Lys Met Ala Met Ser Pro Ala Ser Asp Asp Arg Cys Trp		400
405	410	415
Asn Gly Ile Ser Lys Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly		
420	425	430
Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys		
435	440	445
Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr		
450	455	460
Asn Arg Leu Arg Gly Ala Tyr Gly Gly Asn Asp Val Asp Phe Gln Asp		
465	470	475
Ala Ser Asp Asp Gly Ser Gly Ser Gly Gly Gly Cys Pro Asp		480
485	490	495
Asp Ala Cys Gly Arg Arg Val Ser Lys Lys Ser Ser Ser Arg Thr		
500	505	510
Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys		
515	520	525
Thr Ser Ala		
530		

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCTGGGAG GTGTCATTGC TGGAGGCCTG GTGGGCCTCA TCTTGCTGT GTGCCTGGTG 60  
GCTTTCATGC TATAC 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCCTAGCAG CTGTCATTGC TGGTGGAGTT ATTGGCTTC TCTTGCAAT TTTTCTTATC 60  
CTGCTGTTGG TG 72

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Leu Ala Ala Val Ile Ala Gly Gly Val Ile Gly Phe Leu Phe Ala  
1 5 10 15  
Ile Phe Leu Ile Leu Leu Leu Val  
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTGTTGATAG CTGTGATTGT CGGCCGTGTG GTGGGAGCCC TCTTGCTGC CTTCCCTGTC 60  
ATGCTGCTCA TCTAC 75

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTGGCAG CTCTGATTGT GGGCGCGTA GTGGGCATCC TCTTCGCCGT TTTCTGATC 60  
CTGCTGCTGG TGTAC 75

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGCCACTC GCCCAGAGCC TCACTACTTC TTTCTGCTCT TCCTGTTCAC CTTGGTCCTT 60  
GCTGCAGCCA GGCCCAGGTG GCGGTAAC TG CCC 93

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Thr Arg Pro Glu Pro His Tyr Phe Phe Leu Leu Phe Leu Phe Thr  
1 5 10 15

Leu Val Leu Ala Ala Ala Arg Pro Arg Trp Arg  
20 25

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGCGACACT GCTCATCCCA GCCATCACGA CTGCTGACGC CGGCTTCTAC CTCTGCGTGG 60  
CCACCAGCCC TGCAAGGCACT GCC 83

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCATGAAGA AGAAGGATGAG AGGCAGTTAC GACTTGGGCA AGAAACCCAT CTACAAAAAA 60  
GCCCCCCACCA ACGAGTTCTA CGCATGA 87

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Gly Lys Lys Pro Ile Tyr Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCCGCCAGC AAGAGCCGGA GCT 23

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGAGGCTCT GGGCGAGTGG GGG 23

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
  
ATAGAGCTCT TGGAACCATG GCGCCTGTCT GCC 33

(2) INFORMATION FOR SEQ ID NO:21:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
  
GGAATTCCAG GTTTTATTAT CTTTTTATC 29

(2) INFORMATION FOR SEQ ID NO:22:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
  
CGTATTGGGC GCCGTGTCAC CAGGGC 26

(2) INFORMATION FOR SEQ ID NO:23:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:  
  
GGCCATGAGC TCCACCACCC TGTTCG 26

(2) INFORMATION FOR SEQ ID NO:24:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:  
  
Leu Gly Lys Lys Pro Ile Tyr Lys Lys 9  
1 5

(2) INFORMATION FOR SEQ ID NO:25:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:  
  
Glu Phe Tyr Ala 4  
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